

FIGURE 1A

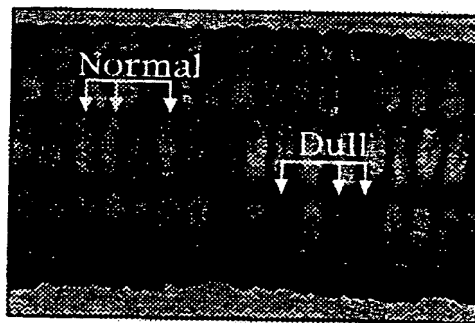


FIGURE 1B

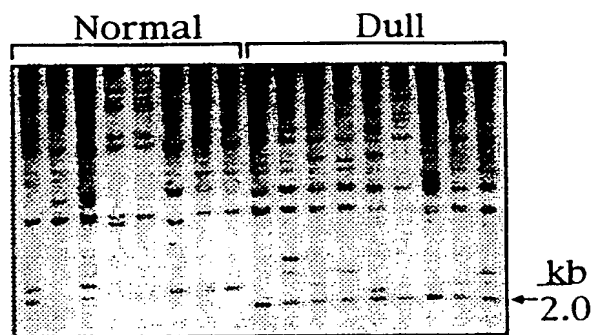


FIGURE 2A



FIGURE 2B

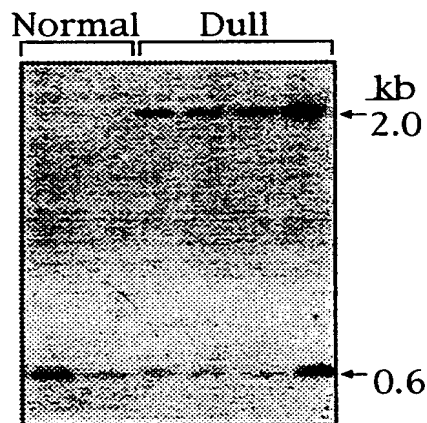


FIGURE 2C

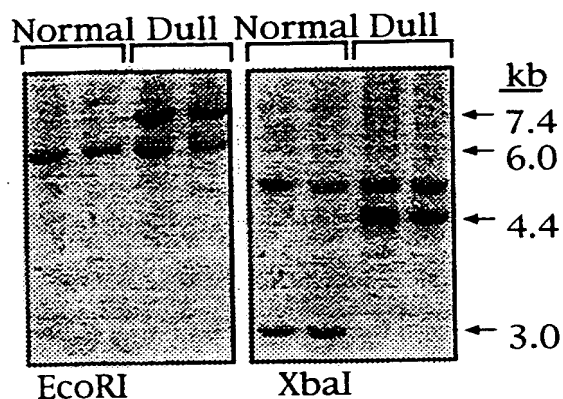
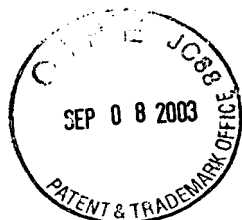


FIGURE 3A

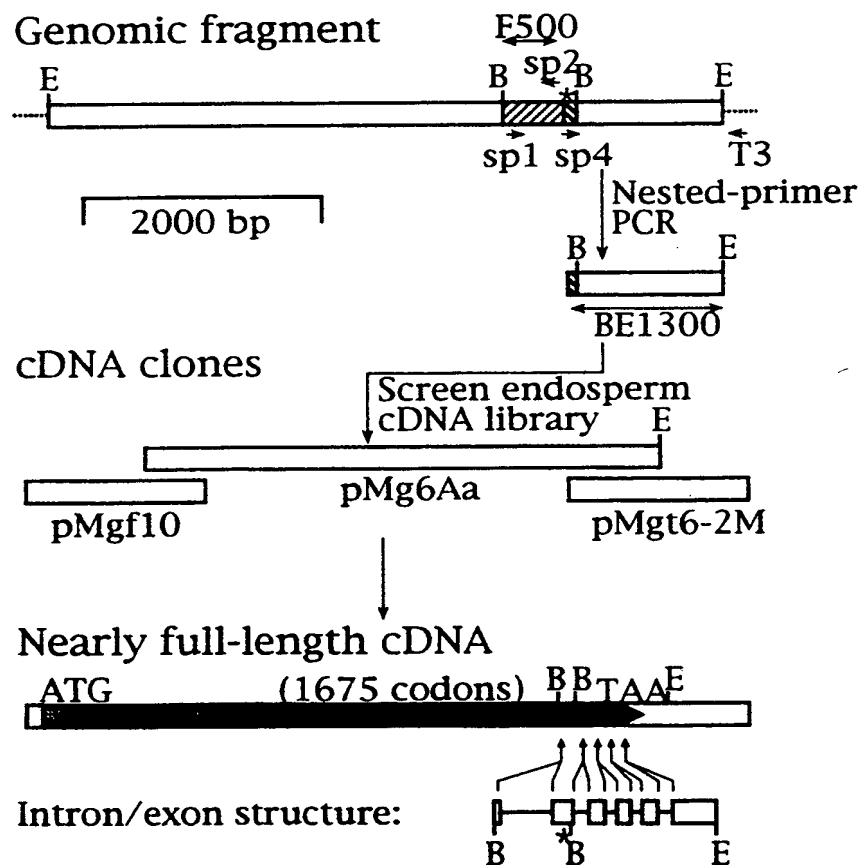


FIGURE 3B

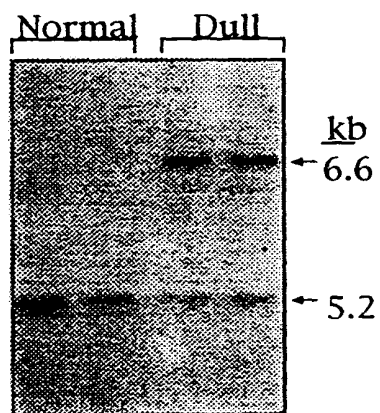


FIGURE 4

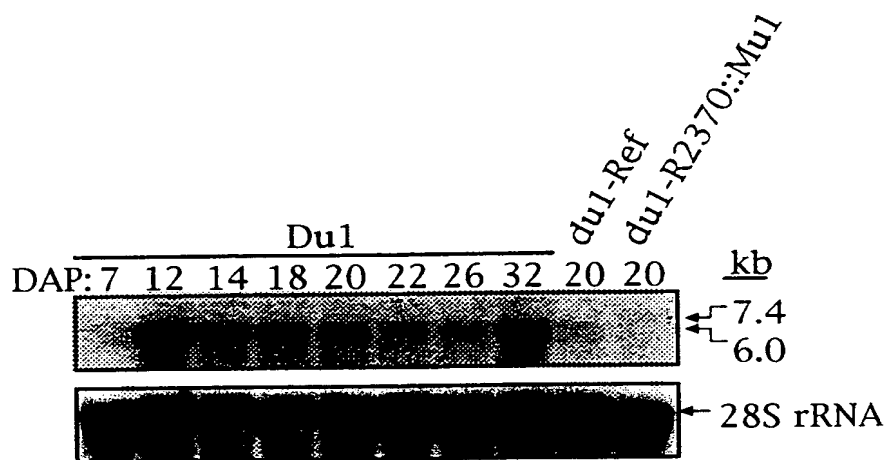


FIGURE 5A

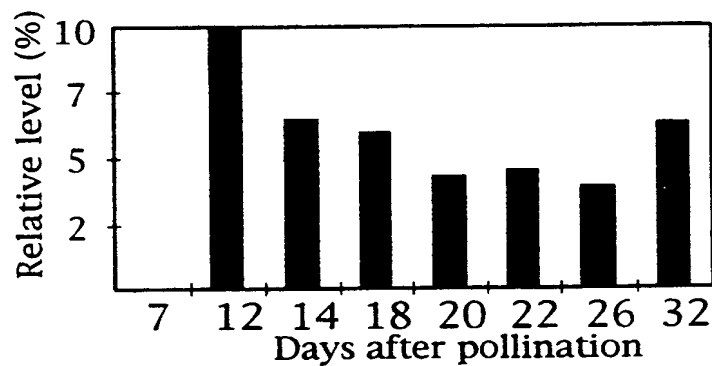


FIGURE 5B

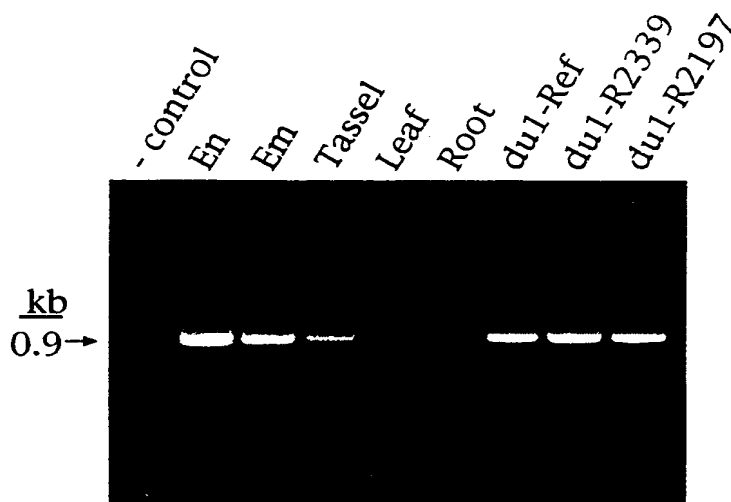
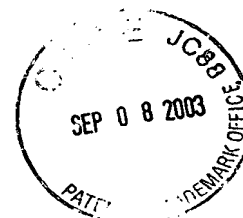


FIGURE 5C

	MEMVLRSQPLCLRSGPVLIFRPTVAGGG	30
DU1	GTQSLLRTRFARRRVIRCVVASPGCPNKRKSRRTASPNVKVAAYSNYAPRLLVSSSKKS	89
DU1	EHDSSRHREETIDTYNGLSGSDAAELTSNRDVEIEVDLQHISEEELPGKVSINASLGE	148
DU1	METVDEAEVEEDKFEVDTSGIVLRNVAVREVPKDEHNAKDV FVVDSSGTAPDNAVEE	207
DU1	VVDEAEVEEDMVDVDILGLDLNNATIEEIDLMEEALENFDVDSPGNASSGRTYGGVDE	266
DU1	LGELPSTSVDCIAINGKRRSLKPKPLPIVRFQEQEQIVLSIVDEEGLIASSCEEQGPVV	325
DU1	DYDKQEEENSTAFDEQKQLTDDFEEGISIVHFPEPNNDIVGSSKFLQKQELDGSYKQD	384
DU1	RSTTGLHEQDQSVVSSHGQDKSIVGVFPQIQYNDQSIAGSHRQDQSIAGAPEQIQSVAG	443
DU1	YIKPNQSI VGSCKQH ELIIPEPKKIESIISYNEIDQSI VGS HKQDKSVVSVPEQIQSIV	502
SS3	MDVPFPLHRSLSCTSVSNAITHLKIKPILGFVSHGTTLSVQSSSWRKDGMVTGVS	56
DU1	SHSKHNSITVDSYRQAESIIIGVPEKVQSITSYDKLDQSI VGS LKQDEPIISVPEKIQSI	561
SS3	FSICANFSGRRRRKVVSTPRSQSSPKGFVPRKPSGMSTQKVKQSNQSGDKESKSTSTKE	115
DU1	VHYTKPNQSI VGLPKQQQSIVHMEPKQSIDGFPKQDLSIVGTSNEFQTKQLATVGT HD	620
SS3	SEISNQKTVEARVETSDDDTKGVVRDHKFLEDEDEINGSTKSLMSPPVRVSSQFVESEE	174
DU1	GLLMKGVEAKETSQKTEGDTLQATFNVDNLSQKQKGLTKEADEITIEKINDEDLVMIE	679
SS3	TGGDDKDAVKLNKSKRSEESGFIIDSUIREQSGSQGFIENASSKGS HAVG TKLYEILQVD	233

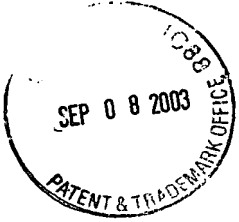
FIGURE 6A-1



DU1	EQKSIAMNEEQTI	VEIGIDKAKFL	HLSEESSW	DENEVGII	EAD	EQYE	738
SS3	VEPQQLKENNAGN	VEYKGPVASK	LEITKASDVETES	NEIDDL	DTNSFFK	SDLEDE	292
DU1	VDETSMTSECI	IQESPNDLDPQALWSMLQEL	AEKNYS	LNK	LFTY	PDVLKADSTIDLY	797
SS3	PLAAGTVETCI	SSNLRLRLEMEANLRRQAIER	LAENL	LOQIR	LECFE	EMVVPDEDEVEIF	351
DU1	FNRLSAVANE	PDVLTKGAFN	GKMRFF	TEK	LHKSEL	AGDWM	856
SS3	LNRLSLTLKNES	DVLTMGAENEMRYR	SETTRL	TETHL	NGDWM	SKIHVPKEAYRADEVF	410
DU1	FNGHTVYENNN	NNDFVIQIESTMDEN	LFEDFL	AEKQRE	LENLANE	EAERRROTDEQRR	915
SS3	FNGQDVYDNN	DGNDESIITVKGGM	QIIDEFENEL	LEEKMR	QEKLAKE	QAERERLAEQORR	469
DU1	MEERADKADR	VQAKVEVEIKK	NKLCNV	GLARAPV	DNLWYIEPT	TGQEA	974
SS3	TEAEKAEI	FADRAQAK	EEAAKKKVL	RELMVK	ATKTRD	ITWYIEPSEFKOEDKVRLYYN	528
DU1	INSRPLVHSTE	IMHGGYNNWIDGLS	FAERLV	HHDKD	CDWMFAD	VVVPERTYVLDWVF	1033
SS3	KSSGPI	SHAKDLMITHGGYNNW	KDGLSIV	KKLVK	SERIDG	DMWYTEVVIDEQALFLDWVF	587
DU1	ADGPPG	SARNYDNNGGHDF	HATLPNNMT	EEFYW	MEEQRTY	TRLOQERRERE	1092
SS3	ADGPEKHA	IAYDNNHRODF	HAIVPNHI	PEELVW	VEEHQIF	FKTLOERRLEAAMRAKV	646
DU1	ERNAKMKA	EMKEKTRM	FLMSQKH	IVYTEPLE	THAGTT	IDVLYNPSNTVLI	1151
SS3	EKTALLKTE	KERTMKSE	LLSOKH	VXYTEPLD	IOAGSSV	TVYYPANTVLANGKPEIWF	705
DU1	CSFNRM	MYPGVLP	PPQKMVQ	AENGSH	LKATV	VPRDAYMDFVFS	1210
SS3	CSFNRM	THRLCPLPPQKM	SPAENGTH	VRATVK	VFLDAYMDFVFS	SEREDGGIFDNKSGM	764
DU1	DYHIPVFG	SIKEPPMH	IVHIAVEMAPI	AKVGG	LDVVTSL	SRAVQDICHNV	1269
SS3	DYHIPVFG	VAKPEPPMH	IVHIAVEMAPI	AKVGG	LDVVTSL	SRAVQDICHNV	823
DU1	GCINLS	NVKNLQIHQSFS	WGGS	SEIN	VWRGL	VEGLQVVFLEPONG	1328
SS3	DCIKMNV	KDFRFFK	NYFMGGTE	IKVMFG	KVEGLSV	VVFLEPONGLE	882

FIGURE 6A-2





1387
941
1446
1000
1505
1059
1564
1118
1623
1177
1674
1230

DU1	RFGFFCRSALEFLLOSGSSFNIIHCHDWSSAPVAVLHKENYAKSSLANARVFTIHNL
SS3	RFGFFCHALEFLLOSGSSFNIIHCHDWSSAPVAVLHKEQYTHYGLSKSRIVFTIHNL
DU1	FGAHHIGKAMRYCDKATTVSNNTYSKEVSGHGAIMPHLGKFGYGLNGIDDPDIWDHYNDNF
SS3	FGADLIGRAMTNADKATTVSPETYSQEVSGNPVIAAPHIHKFHGIIVNGIDDPDIWDHLDNKE
DU1	IPVHYTCENVVEGKRAAKRALQKFGIQQIDMPVVGIVTRLTAQKGIHLIKHAIHRTLE
SS3	IPIPTYISENVVEGKITAAKEALQKFGIQQIDMPVVGIVTRLTHQKGIHLIKHAIWRTLE
DU1	RNGQVLLGSAPDRIQADFVNLANIHLGVNHGQVRISLTYDEPLSHLIYAGSDFILVP
SS3	RNGQVLLGSAPDRVQNNFVNLANQLHISKYNDRARICLTYDEPLSHLIYAGADFILVP
DU1	SIFEPCGLTQLVAMRYGHIPIVRKTGGLFDTVFVDNDKERARDRGLPENGFSFDGADS
SS3	SIFEPCGLTQLVAMRYGSIPIVRKTGGLVDTVFVDNDKERAOQCGLPENGFSFDGADA
DU1	NGVDYALNRATISAMWIDGRSWFHSCLKKVMEOQDWSWNRPALDYIELYRSASKL
SS3	GGVDYALNRATISAMWIDGRWENSLCKKVMEOQDWSWNRPALDYIELYHARKLE

DU1 (SEQ ID NO: 12)

SS3 (SEQ ID NO: 35)

FIGURE 6A-3

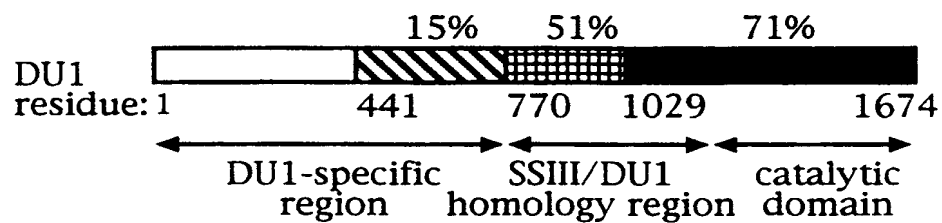


FIGURE 6B

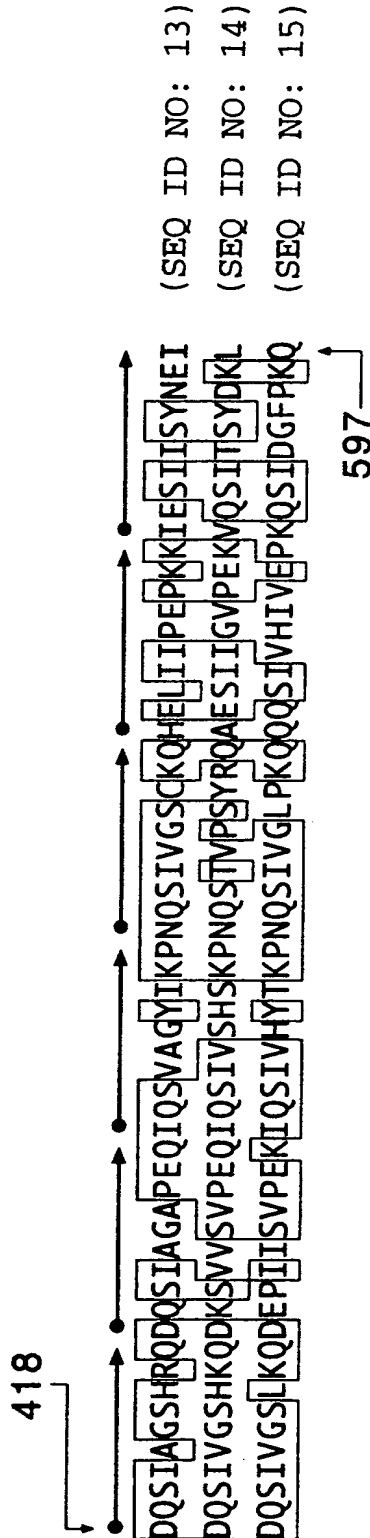
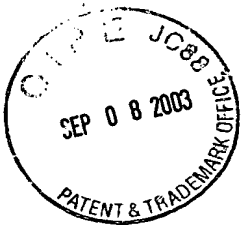
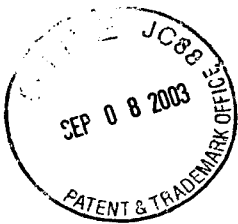


FIGURE 7A



SBE-repeats in DU1:

478	DQSI	VG	SHKQ	487	(SEQ ID NO: 16)
538	DQSI	VG	SLKQ	547	(SEQ ID NO: 17)
	6/6 match				
448	NQSI	VG	SCKQ	457	(SEQ ID NO: 18)
568	NQSI	VG	LPKQ	577	(SEQ ID NO: 19)
418	DQSI	AG	SHRQ	427	(SEQ ID NO: 20)
428	DQSI	AG	APEQ	437	(SEQ ID NO: 21)
404	DKSI	VG	VPQQ	413	(SEQ ID NO: 22)
598	DLSI	VG	NEFQ	607	(SEQ ID NO: 23)
	5/6 match				

FIGURE 7B-1



SBEI family:

Maize SBEI	(SEQ ID NO: 24)
Pea SBEII	(SEQ ID NO: 25)
Wheat SBEI	(SEQ ID NO: 26)

529	*	*	553
KCIAYAESH	DQSIVG	DKTIAFWLMD	
KCVSYAESH	DQSIVG	DKTIAFWLMD	
KCIAYAESH	DQSIVG	DKTMAFWLMD	

6/6 match

SBEII family:

Maize SBEIIa	(SEQ ID NO: 27)
Maize SBEIIb	(SEQ ID NO: 28)
Pea SBEI	(SEQ ID NO: 29)

572	*	*	596
KCVTYCESH	DQALVG	DKTIAFWLMD	
KCVTYAESH	DQALVG	DKTIAFWLMD	
KCVVYCESH	DQALVG	DKTLAFWLMD	

4/6 match

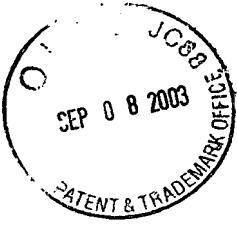
Glycogen branching enzymes:

Yeast GLC3	(SEQ ID NO: 30)
Human liver	(SEQ ID NO: 31)

477	*	*	501
KVVAICESH	DQALVG	DKSLAFWLMD	
KCIAYAESH	DQALVG	DKTLAFWLMD	

4/6 match

FIGURE 7B-2



150 →

ETVDEAEVEEDK	--	FEVD	TS	GI	VL	RN	VA	VR	(SEQ ID NO: 32)
E - VD	PKDEHNAK	DV	FV	VD	SG	TAP	DNA	AVE	(SEQ ID NO: 33)
EVVDEAEVEEDM	--	VD	VD	IL	GL	DL	LN	ATI	(SEQ ID NO: 34)

← 233

FIGURE 7C

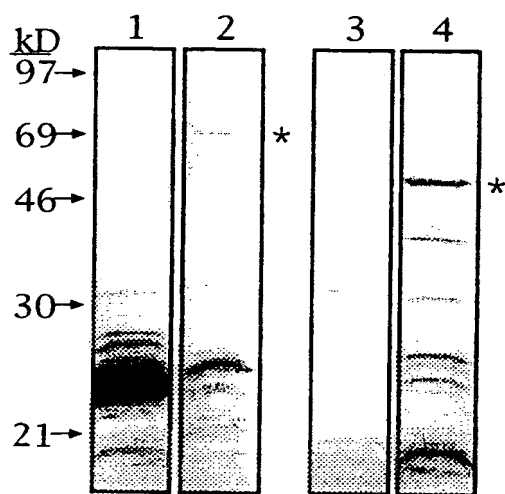


FIGURE 8

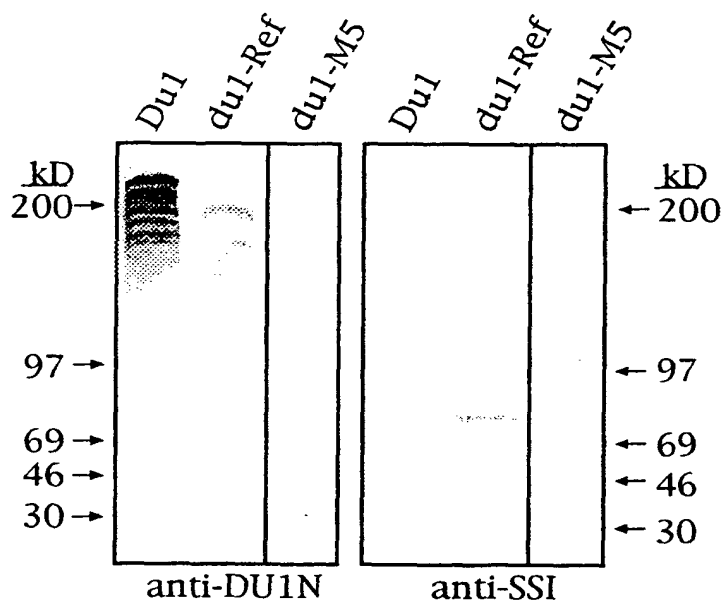


FIGURE 9A

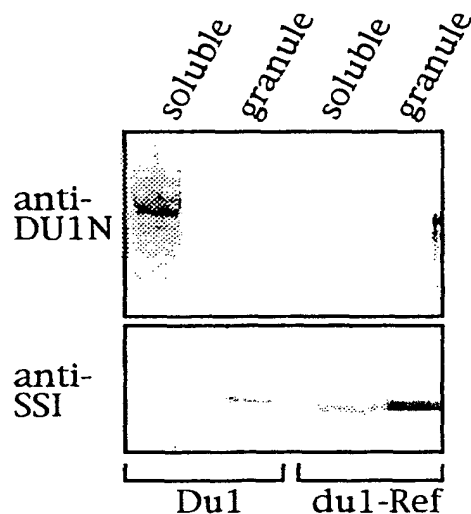


FIGURE 9B

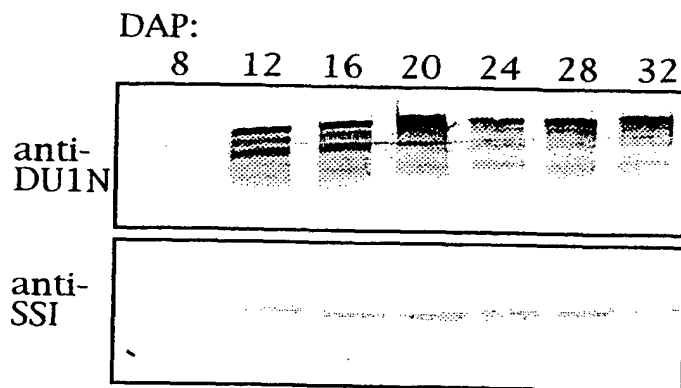


FIGURE 9C

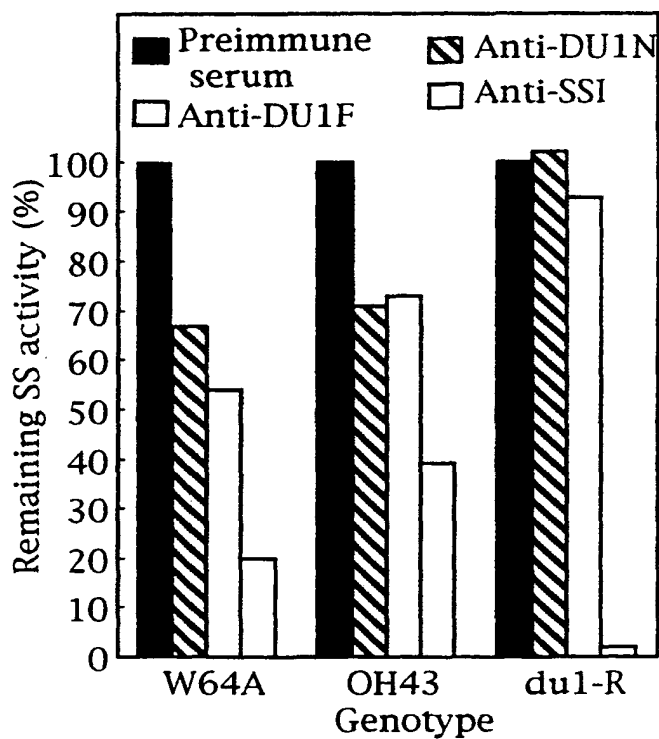


FIGURE 10

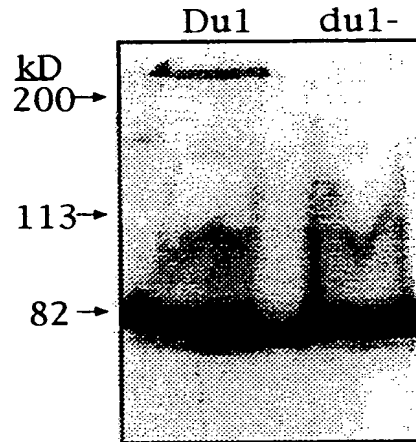


FIGURE 11A

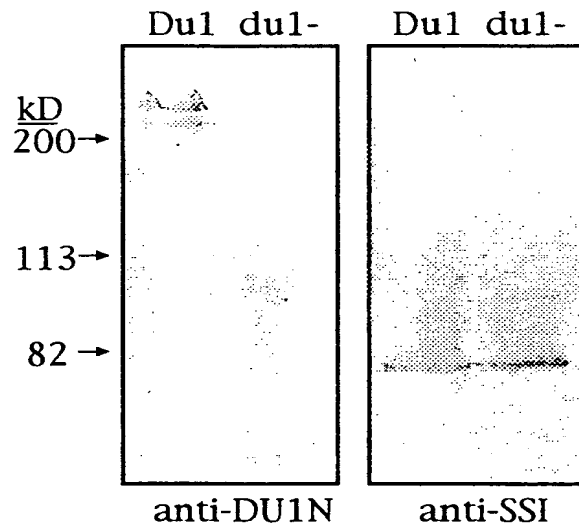


FIGURE 11B

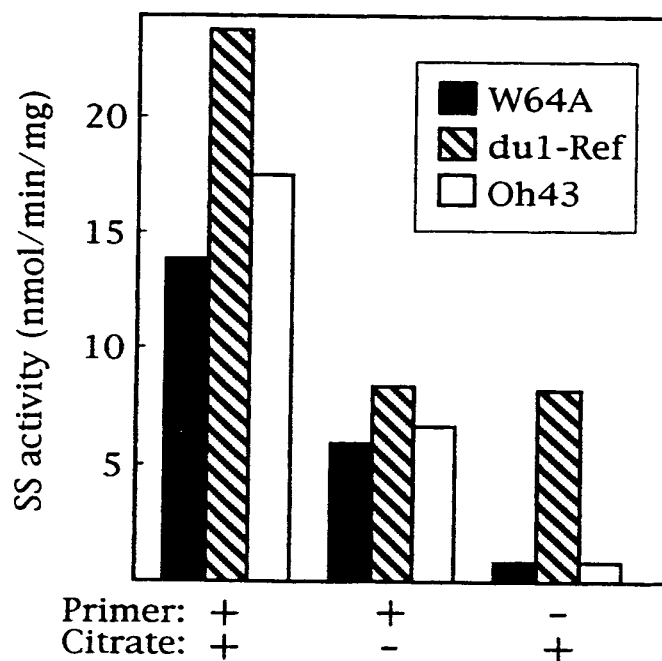


FIGURE 12